

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 23:03:11 ; Search time 1328.9 Seconds

(without alignments)
921.325 Million cell updates/sec

Title: US-10-043-573-57

Sequence: 1 TCCTTACGCTTCATGAGCGCA.....CGGCTGCTCATGAGTCTCC 41

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlu:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estum:*
16: em_estcom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_pig:*
27: em_gss_vil:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	95.1	418	BZ513765	BZ513765 BOMQF58TF
2	39	95.1	554	BG543860	BG543860 E1595 CH1
3	39	95.1	609	CD836743	CD836743 BN45_049M
4	39	95.1	692	BZ026652	BZ026652 ce154h01.

5	39	95.1	695	14	CD836545	CD836545 BN45_049B
6	39	95.1	729	14	CD837127	CD837127 BN45_051C
7	37.4	91.2	510	9	AV525264	AV525264 AV525264
8	37.4	91.2	519	14	T43079	T43079 6342 Lambda
9	37.4	91.2	679	9	AV822338	AV822338 AV822338
10	37.4	91.2	681	13	BH636585	BH636585 BOMBF55TF
11	35.8	87.3	844	28	BH679886	BH679886 BOMBF55TF
12	34.8	84.9	400	14	T41914	T41914 5177 Lambda
13	34.2	83.4	552	28	BZ452017	BZ452017 BOMHM24TF
14	32.6	79.5	237	28	BZ662189	BZ662189 SALK_0256
15	32.6	79.5	373	28	BH813089	BH813089 SALK_0636
16	32.6	79.5	574	9	AU239055	AU239055 AU239055
17	31	75.6	155	28	BH813082	BH813082 SALK_0636
18	28.6	69.8	554	12	BH563044	BH563044 BOMBF55TF
19	27.4	66.8	427	9	AV409658	AV409658 AV409658
20	27.4	66.8	498	12	BH117863	BH117863 L1NEST371
21	27.4	66.8	634	10	AW720138	AW720138 L1NEST154
22	27.4	66.8	670	10	AW720608	AW720608 L1NEST204
23	25.8	62.9	278	9	AV409319	AV409319 AV409319
24	24.8	60.5	646	14	CF450636	CF450636 EST666981
25	24.6	60.0	415	28	BH214235	BH214235 SALK_0104
26	24.6	60.0	494	9	AV525554	AV525554 AV525554
27	24.4	59.5	594	14	CB429996	CB429996 605850 MA
28	23.8	58.0	766	14	CB837022	CB837022 IPCGX13
29	23.8	58.0	766	14	CB837022	CB837022 EST471938
30	23.8	58.0	766	14	CB837022	CB837022 BOMH11TR
31	23.6	57.6	363	29	CG360855	CG360855 BOMH11TR
32	23.6	57.6	699	28	BZ014648	BZ014648 oem74b10.
33	23.4	57.1	628	14	CA483454	CA483454 LUP12010H
34	23.4	57.1	722	29	CE096697	CE096697 LUP12010H
35	23	56.1	293	10	BH511371	BH511371 BB511371
36	23	56.1	428	14	N32472	N32472 YX79C11.X1
37	23	56.1	907	10	BE782561	BE782561 601465851
38	22.8	55.6	162	28	AZ889138	AZ889138 RPCI-24-1
39	22.8	55.6	683	14	CB453647	CB453647 709528 MA
40	22.8	55.6	769	29	CG349119	CG349119 OGIC888TH
41	22.8	55.6	954	29	CG352400	CG352400 OG6A117TC
42	22.6	55.1	421	28	AQ034106	AQ034106 1(3)S2149
43	22.6	55.1	547	12	BZ530357	BZ530357 BZ530357
44	22.6	55.1	577	12	BZ000834	BZ000834 BZ000834
45	22.6	55.1	578	9	AJ457247	AJ457247 AJ457247

ALIGNMENTS

RESULT 1
BZ513765/c 418 bp DNA linear GSS 16-DEC-2002
BOMQF58TF BO_2_3 KB Brassica oleracea genomic clone BOMQF58,
DEFINITION genomic survey sequence.
ACCESSION BZ513765
VERSION BZ513765.1 GI:27040986
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1 (bases 1 to 418)
Town,C.D., Van Aken,S., Uteerback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOMQF58TF
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TP
Class: sheared ends.